

Copyright (c) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: November 6, 2004, 19:24:00 ; Search time 93.625 Seconds
43.019 Million cell updates/sec

Title: US-10-618-644-2

Perfect score: 42

Sequence: 1 PNNKBFQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:
1: uniprot_uniprot:
2: uniprot_trembl:
*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	Q8QKT2	42	100.0	328	2	Q8QKT2 influenza a
2	Q8QKT3	42	100.0	328	2	Q8QKT3 influenza a
3	Q8QKT4	42	100.0	328	2	Q8QKT4 influenza a
4	Q8QKT5	42	100.0	328	2	Q8QKT5 influenza a
5	Q8QKT6	42	100.0	328	2	Q8QKT6 influenza a
6	Q8QKT7	42	100.0	328	2	Q8QKT7 influenza a
7	Q8QKT8	42	100.0	328	2	Q8QKT8 influenza a
8	Q6DM43	42	100.0	363	2	Q6DM43 influenza a
9	Q6DME8	42	100.0	363	2	Q6DME8 influenza a
10	GLC1_SOYBN	42	100.0	481	1	P11828 Glycine max
11	Q852U5	42	100.0	481	2	Q852U5 Glycine max
12	Q852U4	42	100.0	482	2	Q852U4 Glycine max
13	GLC2_SOYBN	42	100.0	485	1	P04405 Glycine max
14	BAC78523	42	100.0	495	1	BAC78523 Glycine max
15	GLC1_SOYBN	42	100.0	495	2	BAC78522 Glycine max
16	BAC78522	42	100.0	495	2	P17002 influenza a
17	HEMA_IAHUR	42	100.0	565	1	Q8igt9 influenza a
18	Q8QKT9	39	92.9	328	2	Q8w6f6 influenza a
19	Q8V6Y9	37	88.1	211	2	Q9w8f7 influenza a
20	Q786K6	37	88.1	236	2	Q9w8f1 influenza a
21	Q786K7	37	88.1	236	2	Q786K7 influenza a
22	Q786L2	37	88.1	236	2	Q786L2 influenza a
23	Q786L3	37	88.1	236	2	Q786L3 influenza a
24	Q9w8f7	37	88.1	236	2	Q9w8f7 influenza a
25	Q9w8f1	37	88.1	236	2	Q9w8f1 influenza a
26	Q7TCQ6	37	88.1	281	2	Q7TCQ6 influenza a
27	Q7TCQ8	37	88.1	281	2	Q7TCQ8 influenza a
28	Q7TCR5	37	88.1	281	2	Q7TCR5 influenza a
29	Q7TCQ3	37	88.1	281	2	Q7TCQ3 influenza a
30	Q7TCT4	37	88.1	281	2	Q7TCT4 influenza a
31	Q91LS8	37	88.1	281	2	Q91LS8 influenza a

RESULT 1

Q8QKT2 PRELIMINARY; PRT; 328 AA.
ID Q8QKT2
AC Q8QKT2;
DT 01-JUN-2002 (TREMBREL. 21, Created)
DT 01-JUN-2002 (TREMBREL. 21, Last sequence update)
DT 01-MAR-2004 (TREMBREL. 26, Last annotation update)
DE Hemagglutinin (Fragment)
OS Influenza A virus (A/Finland/665/99 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza viruses A; H3N2 subtype.
OX NCBI_TaxID=185997;
RN [1]
RL Sequence from N.A.
RP MEDLINE:22290278; PubMedID=12403110;
RX Pyhala R., Ikonen N., Hämpon M., Santanen R., Tervahauta R.;
RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9."
RT Epidemiol. Infect. 129:347-353 (2002).
CC -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
EMBL; AF42466; AAU77312-1.
CC -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR GO:0019031; C-terminal envelope IEA.
DR InterPro: IPR008980; viral infectious cycle; IEA.
DR GO:00019038; capsid; IEA.
DR InterPro: IPR001364; Hemagglutin.
DR InterPro: IPR000149; Hemagglutin-1.
DR Pfam: PF00509; Hemagglutinin_1.
DR PRINTS: PR00310; HEMAGGLUTN1.
DR PRINTS: PR00029; HEMAGGLUTN12.
DR ProDom: PD000225; Hemagglutin_1.
DR Envelope protein; Glycoprotein; Hemagglutin.
FT NON_TER 1
FT NON_TER 328 AA; 36350 MW; D169D8501D885C55 CRC64;
SQ SEQUENCE 328 AA; 36350 MW;

Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Prod. No. 6.7%;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKBFQ 7
Db 289 PNNKBFQ 295

RESULT 2

Q8QKT3 PRELIMINARY; PRT; 328 AA.
ID Q8QKT3
AC Q8QKT3;
DT 01-JUN-2002 (TREMBREL. 21, Created)

01-JUN-2002 (TREMBLref. 21, Last sequence update)	DR	InterPro; IPR001364; Hemagglutinin.
01-MAR-2004 (TREMBLref. 26, Last annotation update)	DR	InterPro; IPR001449; Hemagglutinin.
Hemagglutinin (Fragment)	DR	PF00509; HEMAGGLUTN1.
DE	DR	PRINTS; PR00330; HEMAGGLUTN1.
Influenza A virus (A/Finland/659/99/H3N2)).	DR	PRINTS; PR00129; HEMAGGLUTN12.
OS	DR	ProdDom; PD000225; Hemagglutin; 1.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;	KW	Envelope protein; Glycoprotein; Hemagglutinin.
OC	FT	NON_TER 1
Influenzavirus A; H3N2 subtype.	FT	328 MW; 9B9FD24DBE01PCFE CRC64;
NCBI_TaxID=185995;	SQ	SEQUENCE 328 AA; 36228 MW;
[1]		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.		
CCR		
EMBL; AF442465; AAL77311.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR008380; Capsid; hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
InterPro; IPR000449; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185994;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8EBAD94DAB14F35B CRC64;		
SQ		
SEQUENCE 328 AA; 36224 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.		
CCR		
EMBL; AF442463; AAL77309.1.		
DR		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR		
PFAM; PF00509; HEMAGGLUTN1.		
DR		
PRINTS; PR00330; HEMAGGLUTN1.		
DR		
PRINTS; PR00329; HEMAGGLUTN12.		
DR		
ProdDom; PD000225; Hemagglutin; 1.		
KW		
Envelope protein; Glycoprotein; Hemagglutinin.		
NCBI_TaxID=185995;		
[1]		
NON_TER 1		
FT		
NON_TER 328 MW; 8D78C94DBE6A8B CRC64;		
SQ		
SEQUENCE 328 AA; 36251 MW;		
SEQUENCE FROM N.A.		
RP		
MEDLINE=22290278; PubMed=12403110;		
RX		
Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;		
RA		
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses		
RR		
isolated from conscripts receiving influenza vaccine prior to the		
epidemic season of 1998/9.";		
RT		
Epidemiol. Infect. 129:347-353 (2002).		
RL		
-i- FUNCTION: Hemagglutinin is responsible for attaching the virus to		
cell receptors and for initiating infection (By similarity).		
CC		
-i- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains		
CCC		
(HA1 and HA2) linked by a disulfide bond (By similarity).		
CC		
-i- SIMILARITY: Belongs to the influenza viruses hemagglutinin.		
CCR		
EMBL; AF442464; AAL77310.1.		
DR		
GO; GO:0019031; C: viral envelope; IEA.		
DR		
GO; GO:0019058; P: viral infectious cycle; IEA.		
DR		
InterPro; IPR003880; Capsid_hemag.		
DR		
InterPro; IPR001364; Hemagglutin.		
DR	</	

DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-MAR-2004 (TREMBLrel. 21, Last annotation update)
 DE Hemagglutinin (Fragment).
 OS Influenza A virus (A/Finland/657/99 (H3N2)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H3N2 subtype.
 OX NCBI_TaxID=185993;
 RN [1]
 RP SEQUENCE FROM N.A. MEDLINE=22290278; PubMed=12403110;
 RX Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;
 RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
 isolated from conscripts receiving influenza vaccine prior to the
 epidemic season of 1998/9.",
 RT Epidemiol. Infect. 129:347-353 (2002).
 CC -I- FUNCTION: Hemagglutinin is responsible for attaching the virus to
 cell receptors and for initiating infection (By similarity).
 CC -I- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
 (HA1 and HA2) linked by a disulfide bond (By similarity).
 CC -I- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
 DR EMBL; AF42462; AU77300.1;
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0019058; P:viral infection cycle; IEA.
 DR InterPro; IPR00980; Capsid; hemag.
 DR InterPro; IPR001364; Hemagglutin.
 DR InterPro; IPR00149; Hemagglutin_1.
 DR Pfam; PF00509; Hemagglutinin_1.
 DR PRINTS; PR00330; HEMAGGLUTIN12.
 DR PRINTS; PR00329; HEMAGGLUTIN12.
 DR ProDom; PD00025; Hemagglutin_1.
 DR Envelope protein; Glycoprotein; Hemagglutinin.
 FT NON_TER 1
 FT NON_TER 328 328 AA; 36254 MW; D014B94DABA93F7 CRC64;
 SQ SEQUENCE 328 AA; 36254 MW; D014B94DABA93F7 CRC64;
 Query Match 100.0%; Score 42; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PNNKPFQ 7
 Db 289 PNNKPFQ 295

RESULT 7
 Q8QKT8 PRELIMINARY; PRT; 328 AA.
 ID Q8QKT8; PRELIMINARY; PRT; 328 AA.
 AC Q8QKT8; PRELIMINARY; PRT; 328 AA.
 DR Q8QKT8; PRELIMINARY; PRT; 328 AA.
 DR 01-JUN-2002 (TREMBLrel. 21, Created)
 DR 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DR 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DR Hemagglutinin (Fragment).
 OS Influenza A virus (A/Finland/656/99 (H3N2)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H3N2 subtype.
 OX NCBI_TaxID=185991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22290278; PubMed=12403110;
 RA Pyhala R., Ikonen N., Haapaa M., Santanen R., Tervahauta R.;
 RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
 isolated from conscripts receiving influenza vaccine prior to the
 epidemic season of 1998/9".
 RL -I- FUNCTION: Hemagglutinin is responsible for attaching the virus to
 cell receptors and for initiating infection (By similarity).
 CC -I- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
 (HA1 and HA2) linked by a disulfide bond (By similarity).
 CC -I- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
 DR EMBL; AF42460; AU77306.1;
 DR GO; GO:0019031; C:viral envelope; IEA.
 DR GO; GO:0019058; P:viral infection cycle; IEA.
 DR InterPro; IPR00980; Capsid; hemag.
 DR InterPro; IPR001364; Hemagglutin.
 DR Pfam; PF00509; Hemagglutinin_1.
 DR PRINTS; PR00330; HEMAGGLUTIN12.
 DR PRINTS; PR00329; HEMAGGLUTIN12.
 DR ProDom; PD00025; Hemagglutin_1.
 DR Envelope protein; Glycoprotein; Hemagglutinin.
 FT NON_TER 1
 FT NON_TER 328 328 AA; 36254 MW; D014B94DABA93F7 CRC64;
 SQ SEQUENCE 328 AA; 36254 MW; D014B94DABA93F7 CRC64;
 Query Match 100.0%; Score 42; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PNNKPFQ 7
 Db 289 PNNKPFQ 295

RESULT 8
 Q6DN43 PRELIMINARY; PRT; 363 AA.
 ID Q6DN43 PRELIMINARY; PRT; 363 AA.

```

AC 06DM43 ;          01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DB Hemagglutinin (Fragment).;
OS Influenza A virus (A/Lyon/1803/93 (H3N2)).;
VIRUSES: ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OC NCBI_TaxID=282947;
OX [1] _TaxID=282947;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A/Lyon/1803/93;
RA Smith D.J., Lapedes A.S., de Jong J.C., Bestebroer T.M.,
RA Osterhaus A.D.M.E., Fouchier R.A.M. ;
RT "Mapping the Antigenic and Genetic Evolution of Influenza Virus." ;
SCIENCE 0-0-0(2004)
RL EMBL; AY661169; AAT64844.1; -
RL NON_TER 363 363
FT SEQUENCE 363 AA; 40073 MW; 17B27B34AEAC034C CRC64;
SQ 0;

RESULT 9
Q6DM88
ID Q6DM88
PRIMINARY;
PRT; 363 AA.
AC Q6DM88;
DT 01-OCT-2004 (TREMBLrel. 28, Created)
DT 01-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DR AY661064; AAT64739.1;
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Singapore/53/89 (H3N2)) .
VIRUSES: ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OC NCBI_TaxID=282856;
OX [1] _TaxID=282856;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=A/Singapore/53/89;
RA Smith D.J., Lapedes A.S., de Jong J.C., Bestebroer T.M.,
RA Osterhaus A.D.M.E., Fouchier R.A.M. ;
RT "Mapping the Antigenic and Genetic Evolution of Influenza Virus." ;
SCIENCE 0-0-0(2004)
RL EMBL; AY661064; AAT64739.1; -
RL NON_TER 363 363
FT SEQUENCE 363 AA; 40181 MW; B666EDDB15B94BA86 CRC64;
SQ 0;

RESULT 10
GLC3_SOYBN
ID GLC3_SOYBN
STANDARD;
PRT; 481 AA.
AC P11828;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glycinin G3 precursor [Contains: Glycinin A subunit; Glycinin B subunit];
DE Name=GY3;
GN Glycinin max (Soybean).
OS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


```

OC	SPERMATOPHYTA; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC	NCBI_TaxID=3847;
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Darje. TISSUE=Leaf;
RX	MEDLINE-89226500; PubMed=2740231;
RA	Nielsen N.C., Dickinson C.D., Cho T.-J., Thanh V.H., Scallan B.J.,
RA	Fischer R.L., Nielsen T.L., Drews G.N., Goldberg R.B.;
RA	"Characterization of the Glycinin gene family in soybean.";
RT	"The Glycinin Gy3 gene from soybean.";
RL	Plant Cell 1:313-328 (1989).
RL	CC -1- FUNCTION: Glycinin is the major seed storage protein of soybean.
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond.	
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.	
CC	DISCUSSION OF SEQUENCE.
RX	MEDLINE-92393391; PubMed=2485233;
RA	Nielsen N.C., Dickinson C.D., Cho T.-J., Thanh V.H., Scallan B.J.,
RA	Fischer R.L., Nielsen T.L., Drews G.N., Goldberg R.B.;
RA	"Characterization of the Glycinin gene family in soybean.";
RT	"The Glycinin Gy3 gene from soybean.";
RL	Plant Cell 1:313-328 (1989).
RL	CC -1- FUNCTION: Glycinin is the major seed storage protein of soybean.
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond.	
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL: X15123; CAA33217.1; -.
DR	PIR: S04605; S04605.
DR	HSSP: P04776; 1FXZ.
DR	IntersPro: IPR00604; Cupin.
DR	InterPro: IPR007113; Cupin region.
DR	InterPro: IPR011051; RmLC1-like_cupin.
DR	InterPro: IPR006044; Seedstore_11s.
DR	Pfam: PF00190; Cupin; 2.
DR	PRINTS: PR00439; 11SGLOBULIN.
DR	PROSITE: PS00035; 11S SEED STORAGE; 1.
KW	Multigene family; Seed storage protein; Signal.
FT	SIGNAL 1 21 Glycinin A subunit.
FT	CHAIN 22 296 Glycinin B subunit.
FT	CHAIN 297 476
FT	PROPEP 477 481
FT	DISULFID 107 303 Interchain (By similarity).
SQ	SEQUENCE 481 AA; 54241 MW; 5F5C3148DF6241A7 CRC64;
Query	Match 100.0%; Score 42; DB 1; Length 481;
Best Local Similarity	100.0%; Pred. No. 9 9;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 PNNKPKPQ 7
Db	57 PNNKPKPQ 63
RESULT 11	
Q852U5	PRELIMINARY;
ID	PRT;
AC	481 AA.
DT	01-JUN-2003 (TRIMBLE). 24, [Created]
DT	01-JUN-2003 (TRIMBLE). 24, [Last sequence update]
DT	01-OCT-2003 (TRIMBLE). 25, [Last annotation update]
DE	Glycinin AlkB2-445
DE	Glycinic max (Soybean).
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC	NCBI_TaxID=3847;
RN	

CC -!- FUNCTION: Glycinin is the major seed storage protein of soybean.
 CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond.
 CC -!- SIMILARITY: Belongs to the 11S seed storage protein (Globulins)
 CC family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; X15122; CAA33216.1; -.
 DR EMBL; D00216; BAA00154.1; -.
 DR EMBL; Y00398; CAA68460.1; -.
 DR EMBL; X02066; CAA26575.1; -.
 DR EMBL; X02646; AAA33963.1; -.
 DR EMBL; X53404; CAA37480.1; -.
 DR PIR; A91341; FW5801.
 DR HSSP; P04776; 1PZ2.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR006044; RmlC like_cupin.
 DR InterPro; IPR006044; SeedStorage_11s.
 DR PF00190; Cupin; 2.
 DR PRINTS; PR00439; 11SGBOLIN.
 DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
 DR Direct protein sequencing; Multigene family; Seed storage protein;
 KW SIGNAL.
 FT SIGNAL 1 18 Glycinin A2 subunit.
 FT CHAIN 19 296 Glycinin B1A subunit.
 FT PROPEP 297 300 Glycinin B1A subunit.
 FT CHAIN 301 480 Glycinin B1A subunit.
 FT PROPEP 481 485 Glycinin B1A subunit.
 FT DISULFID 104 307 Interchain.
 FT VARIANT 103 103 G -> D.
 FT VARIANT 318 318 N -> T.
 FT VARIANT 331 331 I -> V.
 FT VARIANT 413 413 K -> R.
 FT CONFLICT 39 39 D -> N (in Ref. 6).
 FT CONFLICT 39 39 D -> G (in Ref. 5).
 FT CONFLICT 61 61 C -> S (in Ref. 6).
 FT CONFLICT 117 117 R -> C (in Ref. 6).
 FT CONFLICT 343 343 W -> S (in Ref. 6).
 SQ SEQUENCE 485 AA; 54391 MW; 788B459837F77AD8 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 485;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OQ 1 PNNKPFQ 7
 DB 54 PNNKPFQ 60

RA Urade R.; Nakatani H.; "mRNA of Soybean Proglycinin A2B1 Subunit.";
 RT Submitted (JUN 2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB11350; BAC78523.1; -.
 SQ SEQUENCE 485 AA; 54390 MW; 788B459837F77AD8 CRC64;
 Query Match 100.0%; Score 42; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OQ 1 PNNKPFQ 7
 DB 54 PNNKPFQ 60

RESULT 15
 GLC1 SOYBN STANDARD; PRT; 495 AA.
 ID GLC1 SOYBN
 AC P04776;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Glycinin GI precursor [Contains: Glycinin A1A subunit; Glycinin BX subunit].
 GN Name=Gly1;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv; Dare; TISSUE=leaf;
 RX MEDLINE=92393391; PubMed=2485233;
 RA Nielsen N.C.; Dickinson C.D.; Cho T.J.; Thanh V.H.; Scallan B.J.;
 RA Fischer R.L.; Sims T.L.; Drews G.N.; Goldberg R.B.;
 RT "Characterization of the glycinin gene family in soybean.";
 RL Plant Cell 1:313-328 (1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv; Bomminori;
 RX MEDLINE=89294649; PubMed=2740229;
 RA Sims T.L.; Goldberg R.B.;
 RA Fischer R.L.; Sims T.L.; Drews G.N.; Goldberg R.B.;
 RT "The Glycinin Gly1 Gene from soybean.";
 RL Nucleic Acids Res. 17:4386-4386 (1989).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv; Bomminori;
 RX MEDLINE=86041867; PubMed=2997720;
 RA Negoro T.; Momma T.; Fukazawa C.;
 RT "An alternate cDNA encoding a Glycinin A1A subunit precursor of soybean.";
 RL Nucleic Acids Res. 13:6719-6731 (1985).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv; Bomminori;
 RX MEDLINE=86041867; PubMed=2997720;
 RA Negoro T.; Momma T.; Fukazawa C.;
 RT "An alternate cDNA encoding a Glycinin A1A subunit.";
 RL Nucleic Acids Res. 13:6719-6731 (1985).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP Urade R.; Nakatani H.; Nakano C.;
 RT "mRNA of soybean proglycinin A1B1 subunit.";
 RL Submitted (JUN 2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond.
 CC -!- PTM: The precursor is post-translational processed to form a
 CC covalently linked A1A-B1 subunit complex.
 CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
 CC family.
 CC

This SWISS-PROT entry is copyright. It is produced through a collaboration -
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC

SEQUENCE FROM N.A.

RN [1]
 RN SEQUENCE FROM N.A.

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi-sib.ch/announce/> or send an email to license@ebi-sib.ch).

CC EMBL; M36686; AAA3966.1; -
 CC EMBL; X15121; CAAJ3215.1; -
 CC EMBL; X02985; CAAE6723.1; -
 CC PIR; AB113349; BAC78522.1; -
 CC PIR; S109851; S109851.
 DR PDB; 1FVZ; X-ray; A/B/C=20-495.
 DR PDB; 1IUD; X-ray; A/B/C=20-495.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR007113; Cupin_region.
 DR InterPro; IPR011051; RmIC_Like_cupin.
 DR InterPro; IPR016044; Seedstore_118.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PRO0039; 11SGLOBULIN.
 DR PROSITE; PS0005; 11S_SPBD_STORAGE; 1.
 KW 3D-structure; Multigene family; Seed storage protein; Signal.
 PT SIGNAL; 1.
 PT CHAIN; 20 306 Glycinin A1A subunit.
 PT PROTEP; 307 310 Glycinin BX subunit.
 PT CHAIN; 311 490 Glycinin BX subunit.
 PT PROBP; 491 495 Glycinin BX subunit.
 PT DISULFID; 107 317 Interchain (By similarity).
 PT CONFLICT; 42 42 D -> G (in Ref. 3);
 PT CONFLICT; 108 108 P -> S (in Ref. 3);
 PT CONFLICT; 136 136 F -> S (in Ref. 3);
 PT CONFLICT; 360 360 E -> G (in Ref. 3);
 PT TURN; 30 31
 PT STRAND; 39 39
 PT STRAND; 43 47
 PT TURN; 48 49
 PT STRAND; 50 54
 PT TURN; 57 58
 PT HELIX; 60 65
 PT TURN; 66 66
 PT STRAND; 68 74
 PT TURN; 76 77
 PT STRAND; 78 84
 PT TURN; 89 95
 PT STRAND; 97 103
 PT TURN; 105 106
 PT STRAND; 134 137
 PT TURN; 138 139
 PT STRAND; 140 144
 PT TURN; 146 147
 PT STRAND; 149 154
 PT TURN; 160 166
 PT STRAND; 168 169
 PT TURN; 171 172
 PT STRAND; 181 183
 PT TURN; 191 192
 PT HELIX; 193 196
 PT STRAND; 222 223
 PT HELIX; 226 233
 PT TURN; 234 234
 PT HELIX; 237 243
 PT STRAND; 255 257
 PT TURN; 317 318
 PT STRAND; 322 324
 PT HELIX; 333 335
 PT TURN; 336 338
 PT STRAND; 339 344
 PT TURN; 346 348
 PT HELIX; 350 352
 PT STRAND; 353 356
 PT TURN; 359 364
 PT TURN; 366 367

Query Match Score 42; DB 1; Length 495;
 Best Local Similarity 100.0%; Prd. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PNNKPFQ 7
 Db 57 PNNKPFQ 63

Search completed: November 6, 2004, 19:52:48
 Job time : 94.625 secs

THIS PAGE BLANK (USPTO)